

PB 504



PCT10

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,768

DATE: 07/15/2002

TIME: 12:43:36

Input Set : A:\2651.ST25.txt

Output Set: N:\CRF3\07152002\J088768.raw

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3 <110> APPLICANT: KATO, Kaneyoshi
4     MORI, Masaaki
5     SUZUKI, Nobuhiro
6     SHIMOMURA, Yukio
7     TAKEKAWA, Shiro
8     CHOH, Nobuo
10 <120> TITLE OF INVENTION: MCH Antagonists
12 <130> FILE REFERENCE: 2651 USOP
14 <140> CURRENT APPLICATION NUMBER: 10/088,768
C--> 15 <141> CURRENT FILING DATE: 2002-06-25
17 <150> PRIOR APPLICATION NUMBER: PCT/JP00/06376
18 <151> PRIOR FILING DATE: 2000-09-19
20 <150> PRIOR APPLICATION NUMBER: JP 11-266278
21 <151> PRIOR FILING DATE: 1999-09-20
23 <150> PRIOR APPLICATION NUMBER: JP 2000-221055
24 <151> PRIOR FILING DATE: 2000-07-17
26 <160> NUMBER OF SEQ ID NOS: 16
28 <170> SOFTWARE: PatentIn version 3.0
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31 <211> LENGTH: 32
32 <212> TYPE: DNA
C--> 33 <213> ORGANISM: artificial
35 <220> FEATURE:
36 <223> OTHER INFORMATION: primer
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55 <211> LENGTH: 353
56 <212> TYPE: PRT
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59 <400> SEQUENCE: 3
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64 Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg
65           20           25           30

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67 Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
68          35          40          45
70 Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
71          50          55          60
73 Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
74 65          70          75          80
76 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
77          85          90          95
79 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
80          100          105          110
82 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
83          115          120          125
85 Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala
86          130          135          140
88 Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala
89 145          150          155          160
91 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
92          165          170          175
94 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
95          180          185          190
97 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
98          195          200          205
100 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
101          210          215          220
103 Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala
104 225          230          235          240
106 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
107          245          250          255
109 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
110          260          265          270
112 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
113          275          280          285
115 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
116          290          295          300
118 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
119 305          310          315          320
121 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr
122          325          330          335
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125          340          345          350
127 Thr
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133 <213> ORGANISM: rat
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138 gatggccagg ataatctcac attgccgggg tcacctctc gcacagggag tgtctctac      120
140 atcaacatca ttatgccttc cgtgtttggt accatctgtc tcctgggcat cgtgggaaac      180

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142 tccacggtca tctttgctgt ggtgaagaag tccaagctac actggtgcag caacgtcccc 240
144 gacatcttca tcatcaacct ctctgtggtg gatctgctct tcctgctggg catgcctttc 300
146 atgatccacc agctcatggg gaacggcgtc tggcactttg gggaaaccat gtgcaccctc 360
148 atcacagcca tggacgccaa cagtcagttc actagcacct acatcctgac tgccatgacc 420
150 attgaccgct acttggccac cgtccacccc atctcctcca ccaagttccg gaagccctcc 480
152 atggccaccc tggatgctg cctcctgtgg gcgctctcct tcatcagtat caccctgtg 540
154 tggctctacg ccaggctcat tcccttccca gggggtgctg tgggctgtgg catccgcctg 600
156 ccaaaccggg acactgacct ctactggttc actctgtacc agtttttcct ggcctttgcc 660
158 cttccgtttg tggtcattac cgccgcatac gtgaaaatac tacagcgcat gacgtcttcg 720
160 gtggccccag cctcccaacg cagcatccgg cttcggacaa agaggggtgac ccgcacggcc 780
162 attgccatct gtctggtctt ctttgtgtgc tgggcaccct actatgtgct gcagctgacc 840
164 cagctgtcca tcagccgccc gaccctcagc tttgtctact tgtacaacgc ggccatcagc 900
166 ttgggctatg ctaacagctg cctgaacccc tttgtgtaca tagtgcctctg tgagaccttt 960
168 cgaaaacgct tgggtgtgtc agtgaagcct gcagcccagg ggcagctccg cacggtcagc 1020
170 aacgctcaga cagctgatga ggagaggaca gaaagcaaag gcacctgaac tagt 1074
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174 <211> LENGTH: 262
175 <212> TYPE: RNA
176 <213> ORGANISM: rat
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181 uccugcagcc cgggggaucc gccacuagu ucaggugccu uugcuuucug uccucuccuc 120
183 aucagcuguc ugagcguugc ugaccgugcg gagcugcccc ugggcugcag gcuucacuga 180
185 caacaccaag cguuuucgaa agguucacac gagcacuaug uacacaaagg gguucaggca 240
187 gcuguuagca uagcccaagc ug 262
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192 <212> TYPE: DNA
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195 <220> FEATURE:
196 <223> OTHER INFORMATION: primer
198 <400> SEQUENCE: 6
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202 <210> SEQ ID NO: 7
203 <211> LENGTH: 18
204 <212> TYPE: DNA
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207 <220> FEATURE:
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215 <211> LENGTH: 1275
216 <212> TYPE: DNA
217 <213> ORGANISM: human
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222 ggcagcggtc gccaggctac ggaggaagac ccccttccca actgcggggc ttgcgctccg 120
224 ggacaagggtg gcaggcgctg gaggctgccg cagcctgcgt ggggtggaggg gagctcagct 180

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226 cggttgtggg agcaggcgac cggcactggc tggatggacc tggaaagcctc gctgctgccc 240
228 actgggtccca acgccagcaa cacctctgat ggccccgata acctcacttc ggcaggatca 300
230 cctcctcgca cggggagcat ctctacatc aacatcatca tgccttcggt gttcggcacc 360
232 atctgcctcc tgggcatcat cgggaactcc acggtcatct tcgcggtcgt gaagaagtcc 420
234 aagctgcaact ggtgcaacaa cgtccccgac atcttcatca tcaacctctc ggtagtagat 480
236 ctctcttttc tcttgggcat gcccttcatg atccaccagc tcatgggcaa tgggggtgtgg 540
238 cactttgggg agaccatgtg caccctcatc acggccatgg atgccaatag tcagttcacc 600
240 agcacctaca tcttgaccgc catggccatt gaccgctacc tggccactgt ccaccccatc 660
242 tcttccacga agttccggaa gccctctgtg gccacccctgg tgatctgcct cctgtggggcc 720
244 ctctccttca tcagcatcac ccctgtgtgg ctgtatgcca gactcatccc cttcccagga 780
246 ggtgcagtgg gctgcggcat acgcctgccc aaccagaca ctgacctcta ctggttcacc 840
248 ctgtaccagt ttttctggc ctttgccttg cttttgtgg tcatcacagc cgcatacgtg 900
250 aggatcctgc agcgcagtac gtcctcagtg gccccgcct cccagcgcag catccggctg 960
252 cggacaaaga gggtgacccg cacagccatc gccatctgtc tgggtcttctt tgtgtgctgg 1020
254 gcacctact atgtgtaca gctgaccag ttgtccatca gccgcccagc cctcaccttt 1080
256 gtctacttat acaatgcggc catcagcttg ggctatgcca acagctgcct caacccttt 1140
258 gtgtacatcg tgctctgtga gacgttccgc aaacgcttgg tcctgtcggg gaagcctgca 1200
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266 <211> LENGTH: 422
267 <212> TYPE: PRT
268 <213> ORGANISM: human
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276 20 25 30
278 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
279 35 40 45
281 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
282 50 55 60
284 Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
285 65 70 75 80
287 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
288 85 90 95
290 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
291 100 105 110
293 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
294 115 120 125
296 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
297 130 135 140
299 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
300 145 150 155 160
302 Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
303 165 170 175
305 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
306 180 185 190
308 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile

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309          195          200          205
311 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
312          210          215          220
314 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
315 225          230          235          240
317 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
318          245          250          255
320 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
321          260          265          270
323 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
324          275          280          285
326 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
327          290          295          300
329 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
330 305          310          315          320
332 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
333          325          330          335
335 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
336          340          345          350
338 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
339          355          360          365
341 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
342          370          375          380
344 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
345 385          390          395          400
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351          420
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354 <211> LENGTH: 31
355 <212> TYPE: DNA
C--> 356 <213> ORGANISM: artificial
358 <220> FEATURE:
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361 <400> SEQUENCE: 10
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366 <211> LENGTH: 31
367 <212> TYPE: DNA
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370 <220> FEATURE:
371 <223> OTHER INFORMATION: primer
373 <400> SEQUENCE: 11
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378 <211> LENGTH: 33
379 <212> TYPE: DNA
C--> 380 <213> ORGANISM: artificial

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,6,7,10,11,12,13

VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:45 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:193 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:205 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:356 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:368 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:380 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:392 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13